Amendments to the claims

This listing of claims will replace all prior versions and listings of claims in the application.

Listing of claims

1. (Currently amended) A method for determining the predisposition or susceptibility of a human individual to an adverse reaction, a side effect or a variation in response to therapy to a biologically active compound that is metabolized through *UGT1A9* glucuronidation, said method comprising:

- obtaining a nucleic acid sample from said individual; and
- determining the presence of a T^{-275}A substitution ~~polymorphic or haplotypic variation~~ in ~~the~~ nucleotide sequence of *UGT1A9* gene from said nucleic acid sample of said individual~~, said variation comprising: a T^{-275}A substitution~~;

whereby the presence of the T^{-275}A substitution~~polymorphic or haplotypic variation~~ in said nucleotide sequence is indicative of said predisposition or susceptibility.

2. (Original) The method of claim 1, wherein said predisposition is a hereditary predisposition.

3. – 7. (Cancelled)

8. (Previously amended) The method of claim 30, wherein said compound is an anti-cancer agent or an immunosuppressive agent.

9. (Original) The method of claim 8, wherein said anti-cancer agent is a camptothecin or an analog thereof.

10. (Previously amended) The method of claim 9, wherein said camptothecin analog is 7-ethyl-10-[4-(1-piperidino)-1-piperidino] carbonyloxy camptothecin (irinotecan, CPT-11) or 7-ethyl-10-hydroxycamptothecin (SN-38).

11. (Original) The method of claim 8, wherein said immunosuppressive agent is mycophenolic acid (MPA).

12. (Cancelled)

13. (Currently amended) The method of claim 1, wherein said human has a cancer.

14. (Previously amended) The method of claim 13, wherein said cancer is at least one of colorectal cancer, a solid tumor and a hematological cancer.

15. (Previously amended) The method of claim 1, wherein said nucleic acid is a DNA or a RNA sample of said individual.

16. – 17. (Cancelled)

18. (Previously amended) The method of claim 31, wherein said $G^{8}A$ missense mutation is associated with a decreased predisposition or susceptibility to an anti-cancer agent.

19. (Previously amended) The method of claim 31, wherein said $G^{8}A$ missense mutation is associated with a decreased responsiveness to an immunosuppressive agent.

20. (Previously amended) The method of claim 31, wherein said $T^{98}C$ missense mutation is associated with an increased adverse reaction to an anti-cancer agent.

21. (Previously amended) The method of claim 1, further comprising determining the presence of a polymorphic or haplotypic variation in the UGT1A7 gene.

22. (Previously amended) The method of claim 21, wherein said polymorphic or haplotypic variation is at least one of a $G^{353}T$ missense mutation, a $T^{397}G$ missense mutation, a $C^{401}A$ missense mutation, a $G^{402}A$ missense mutations, a $G^{427}C$ missense mutation and a $T^{632}C$ missense mutation.

23. (Previously amended) The method of claim 1 or 21, further comprising determining the presence of a polymorphic or haplotypic variation in the UGT1A1gene.

24. (Previously amended) The method of claim 23, wherein said polymorphic or haplotypic variation is a TA_7 mutation in the TATA box.

25. (Withdrawn) An isolated nucleotide sequence comprising at least one nucleotide sequence selected from the group consisting of SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45 SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 52, SEQ ID NO: 53, SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, SEQ ID NO: 58, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, a fragment or the complementary sequences thereof, for determining predisposition to a physiological reaction.

26. (Withdrawn) The nucleotide sequence of claim 25, wherein said sequence is an allelic 6ariant of UGT1A1, UGT1A7 or UGT1A9.

27. (Withdrawn) An isolated amino acid sequence comprising at least one amino acid sequence selected from the group consisting of SEQ ID NO: 69, SEQ ID NO: 70, SEQ ID NO: 71 or a fragment thereof.

28. (Withdrawn) The amino acid sequence of claim 27, wherein said sequence is encoded by a nucleotide sequence comprising at least one sequence selected from the group consisting of SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, a fragment or the complementary sequences thereof.

29. (Withdrawn) The amino acid sequence of claim 27, wherein the expression of said sequence is regulated by a nucleotide sequence comprising at least one sequence selected from the group consisting of SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45 SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 52, SEQ ID NO: 53, SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, SEQ ID NO: 58, SEQ ID NO: 59, a fragment or the complementary sequences thereof.

30. (Previously submitted) The method according to claim 1, wherein said compound is selected from the group consisting of: an anti-cancer agent, an immunosuppressive agent, a carcinogen and a pre-carcinogen.

31. (Currently amended). The method of claim 1, ~~wherein~~ further comprising the step of identifying a further substitution ~~said polymorphic or haplotypic variation is further~~ selected from the group~~s~~ consisting of: a $C^{-2208}T$ substitution, a $C^{-2152}T$ substitution, a $C^{-2141}T$ substitution, a $T^{-1887}G$ substitution, a $T^{-1818}C$ substitution, a $C^{-665}T$ substitution, a $T^{-440}C$ substitution, a $C^{-331}T$ substitution, a $G^{-87}A$ substitution, a $G^{8}A$ missense mutation ($C^{3}Y$) and a $T^{98}C$ missense mutation ($M^{33}T$).

32. (Cancelled)